



SEQUENCE LISTING

<110> Snutch, Terry
NeuroMed Technologies, Inc.

<120> NOVEL HUMAN CALCIUM CHANNELS AND RELATED
PROBES, CELL LINES AND METHODS

<130> 38109-20007.00

<140> US 09/030,482

<141> 1998-02-25

<150> US 60/039,204

<151> 1997-02-28

<160> 33

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 24

<212> DNA

<213> Rat

<400> 1

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<210> 2

<211> 24

<212> DNA

<213> Rat

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aacgtgttct tggctatcgc ggtg

24

<210> 3

<211> 24

<212> DNA

<213> Rat

<400> 3

gtgaaagcac agagcttcta ctgg

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gttaaatacca acgtcttcta ctgg
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aatgtattct tggctatcgc tgtg
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<211> 21

<212> DNA
<213> Rat

<400> 11
atctaygcyr tsatyggsat g
21

<210> 12
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<212> DNA
<213> Rat

<400> 12
atggacaayt tygastaytc
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<210> 13
<211> 168
<212> DNA
<213> Human

<220>
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gtgatcactc tggaaggctg ggtggagatc atgtactacg tgatggatgc tcactccttc
60
tacaacttca tctacttcat cctgcttata ataccctct tgccttgac cccatatggt
120
cttcccagag tgagctcatc cacctcgtca tgcctgactc gacgttca
168

<210> 14
<211> 98
<212> DNA
<213> Human

<220>
<223> Expressed sequence tag H55617

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gatggctcag tactccctgg accttcagaa catcaacctg tcagccatcc gcaccgtgcg
60
cgtcctgagg cccctcaaag ccatcaaccg cgtgccca
98

<210> 15
<211> 94
<212> DNA
<213> Human

<220>
<223> Expressed sequence tag H55223

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catgctggtg atcctgctga actgcgtgac acttggcatg taccagccgt gcgacgacat
60

ggactgcctg tccgaccgct gcaagatcct gcag
94

<210> 16
<211> 123
<212> DNA
<213> Human

<220>
<223> Expressed sequence tag H55544

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gtatctctgg ttacttttagt agccaacact cttggctact cagaccttgg tcccattaaa
60
tccctgcgaa ccttgagagc actaagacct ctaagagctt tgtctagatt tgaaggaatg
120
agg
123

<210> 17
<211> 343
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<221> misc_feature
<222> (1)... (343)
<223> n = A,T,C or G

<400> 17
ttctctccat tgtaggaatg tttctggctg aactgataga aaagtatttt gtgtgccta
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ccctgttncg agtgatccgt cttgccagga ttggccgaat cctacgtctg atcaaaggag
120
caaaggggat cgcacgctg ctctttgctt tgatgatgtc ccttcctgcg ttgtttaaca
180
tcggnctect tcttttctctg gtcattgttca tctacgncat ctttgggatg tccaattttg
240
cctatgttaa gaggggaagt gggatcgatg acatgttnan ctttgagacc tttggcaaca
300
gcatgatctg cctgttccaa attacaacct ctgctggctg gga
343

<210> 18
<211> 5562
<212> DNA
<213> Human

<220>
<221> CDS
<222> (1)... (5562)
<223> Human alpha-1 partial sequence from BAC bK206c7

<400> 18

atg ttt ttc gtc tca gcc aat ccc tgg gtg agt ttc acc agt ttt gat
 48
 Met Phe Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp
 1 5 10 15
 tta aac gtg gcc aat atg gac aac ttc ttc gcc ccc gtt ttc acc atg
 96
 Leu Asn Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met
 20 25 30
 ggc aaa tat tat acg caa ggc gac aag gtg ctg atg ccg ctg gcg att
 144
 Gly Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile
 35 40 45
 cag gct ctg aaa cag ctg atg ttc aaa ttg gtg gcc act gtt gct cga
 192
 Gln Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg
 50 55 60
 aca cat gct aca ccg tca cac atc acg ggt ggt cct gga aca ggg atg
 240
 Thr His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met
 65 70 75 80
 cac acg ggc acc ttc cag gaa gga gct gag cct ggt tca tct cag cac
 288
 His Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His
 85 90 95
 cct gag gca cag gcc acg tat aca gca ggg tgc acc cca gcc ccc acg
 336
 Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr
 100 105 110
 ggc gat ccc acc tgc tgc ttt gtc ctt gac ttg gtg tgc acg tgg ttt
 384
 Gly Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe
 115 120 125
 gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt ggc
 432
 Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly
 130 135 140
 atg tac cag ccg tgc gac gac atg gac tgc ctg tcc gac cgc tgc aag
 480
 Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys
 145 150 155 160
 atc ctg cag gtc ttt gat gac ttc atc ttt atc ttc ttt gcc atg gag
 528
 Ile Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu
 165 170 175
 atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc tac
 576

Met	Val	Leu	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys	Lys	Cys	Tyr
			180					185					190		
ctc	ggg	gac	aca	tgg	aac	cgc	ctg	gat	ttc	ttc	atc	gtc	atg	gca	ggc
624															
Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val	Met	Ala	Gly
		195					200					205			
aac	atc	aac	ctg	tca	gcc	atc	cgc	acc	gtg	cgc	gtc	ctg	agg	ccc	ctc
672															
Asn	Ile	Asn	Leu	Ser	Ala	Ile	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu
	210					215					220				
aaa	gcc	atc	aac	cgc	gtg	ccc	agt	atg	cgg	atc	ctg	gtg	aac	ctg	ctc
720															
Lys	Ala	Ile	Asn	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Asn	Leu	Leu
225					230					235					240
ctg	gac	aca	ctg	ccc	atg	ctg	ggg	aat	gtc	ctg	ctg	ctc	tgc	ttc	ttt
768															
Leu	Asp	Thr	Leu	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe
				245					250					255	
gtc	ttc	ttc	atc	ttt	ggc	atc	ata	ggc	gtg	cag	ctc	tgg	gcg	ggc	ctg
816															
Val	Phe	Phe	Ile	Phe	Gly	Ile	Ile	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu
			260					265					270		
ctg	cgt	aac	cgc	tgc	ttc	ctg	gag	gag	aac	ttc	acc	ata	caa	ggg	gat
864															
Leu	Arg	Asn	Arg	Cys	Phe	Leu	Glu	Glu	Asn	Phe	Thr	Ile	Gln	Gly	Asp
		275					280					285			
gtg	gcc	ttg	ccc	cca	tac	tac	cag	ccg	gag	gag	gat	gat	gag	atg	ccc
912															
Val	Ala	Leu	Pro	Pro	Tyr	Tyr	Gln	Pro	Glu	Glu	Asp	Asp	Glu	Met	Pro
	290					295					300				
ttc	atc	tgc	tcc	ctg	tcg	ggc	gac	aat	ggg	ata	atg	ggc	tgc	cat	gag
960															
Phe	Ile	Cys	Ser	Leu	Ser	Gly	Asp	Asn	Gly	Ile	Met	Gly	Cys	His	Glu
305					310					315					320
atc	ccc	ccg	ctc	aag	gag	cag	ggc	cgt	gag	tgc	tgc	ctg	tcc	aag	gac
1008															
Ile	Pro	Pro	Leu	Lys	Glu	Gln	Gly	Arg	Glu	Cys	Cys	Leu	Ser	Lys	Asp
				325					330					335	
gac	gtc	tac	gac	ttt	ggg	gcg	ggg	cgc	cag	gac	ctc	aat	gcc	agc	ggc
1056															
Asp	Val	Tyr	Asp	Phe	Gly	Ala	Gly	Arg	Gln	Asp	Leu	Asn	Ala	Ser	Gly
			340					345					350		
ctc	tgt	gtc	aac	tgg	aac	cgt	tac	tac	aat	gtg	tgc	cgc	acg	ggc	agc
1104															
Leu	Cys	Val	Asn	Trp	Asn	Arg	Tyr	Tyr	Asn	Val	Cys	Arg	Thr	Gly	Ser
		355					360					365			

gcc aac ccc cac aag ggt gcc atc aac ttt gac aac atc ggt tat gct
 1152
 Ala Asn Pro His Lys Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala
 370 375 380

tgg att gtc atc ttc cag gtg atc act ctg gaa ggc tgg gtg gag atc
 1200
 Trp Ile Val Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Glu Ile
 385 390 395 400

atg tac tac gtg atg gat gct cac tcc ttc tac aac ttc atc tac ttc
 1248
 Met Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe
 405 410 415

atc ctg ctt atc ata agt gag ctc atc cac ctc gtc atg cct gac tgc
 1296
 Ile Leu Leu Ile Ile Ser Glu Leu Ile His Leu Val Met Pro Asp Cys
 420 425 430

agc ttc agc aca gca cag tcc cca aaa tgt caa ggt gat tca ctc cca
 1344
 Ser Phe Ser Thr Ala Gln Ser Pro Lys Cys Gln Gly Asp Ser Leu Pro
 435 440 445

gga gtc gct gct gaa tcc ctg ctg ctg cga gac tct agc tcc tca gtc
 1392
 Gly Val Ala Ala Glu Ser Leu Leu Leu Arg Asp Ser Ser Ser Ser Val
 450 455 460

atc act gat gag gct gca gcc atg gag aac ctc ctg gcg ggc acc tcc
 1440
 Ile Thr Asp Glu Ala Ala Ala Met Glu Asn Leu Leu Ala Gly Thr Ser
 465 470 475 480

aag ggg gat gaa agc tat ctg ctc agg ctg gcc ggc agc caa gtt cac
 1488
 Lys Gly Asp Glu Ser Tyr Leu Leu Arg Leu Ala Gly Ser Gln Val His
 485 490 495

tcc cag gct cag caa atg ctg ggg agg ggg ctg ggc cct gaa agc ctg
 1536
 Ser Gln Ala Gln Gln Met Leu Gly Arg Gly Leu Gly Pro Glu Ser Leu
 500 505 510

gaa act gga gag gag ccc cac tcg tgg agc cct cgg gcc aca agg aga
 1584
 Glu Thr Gly Glu Glu Pro His Ser Trp Ser Pro Arg Ala Thr Arg Arg
 515 520 525

tgg gat ccc caa tgc caa cca ggg cag cct ctc ccc ctt cat ttc atg
 1632
 Trp Asp Pro Gln Cys Gln Pro Gly Gln Pro Leu Pro Leu His Phe Met
 530 535 540

caa gca cag gtg ggc tcc ttc ttc atg atc aac ctg tgc ctc gtt gtc
 1680
 Gln Ala Gln Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
 545 550 555 560

ata gcg acc cag ttc tcg gag acc aag caa cgg gag cac cgg ctg atg
 1728
 Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met
 565 570 575

ctg gag cag cgg cag cgc tac ctg tcc tcc agc acg gtg gcc agc tac
 1776
 Leu Glu Gln Arg Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr
 580 585 590

gcc gag cct ggc gac tgc tac gag gag atc ttc cag tat gtc tgc cac
 1824
 Ala Glu Pro Gly Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His
 595 600 605

atc ctg cgc aag gcc aag cgc cgc gcc ctg ggc ctc tac cag gcc ctg
 1872
 Ile Leu Arg Lys Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu
 610 615 620

cag agc cgg cgc cag gcc ctg ggc ccg gag gcc ccg gcc ccc gcc aaa
 1920
 Gln Ser Arg Arg Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys
 625 630 635 640

cct ggg ccc cac gcc aag gag ccc cgg cac tac cct ctc aca gtc tgg
 1968
 Pro Gly Pro His Ala Lys Glu Pro Arg His Tyr Pro Leu Thr Val Trp
 645 650 655

gaa tcg att ctt ggg agg caa gca gaa gaa tgc acg ctc aga gct gcc
 2016
 Glu Ser Ile Leu Gly Arg Gln Ala Glu Glu Cys Thr Leu Arg Ala Ala
 660 665 670

gcc cac ccg tcc tcg ggt gcc agc cat cca ggc gtg ggc tcg gag gag
 2064
 Ala His Pro Ser Ser Gly Ala Ser His Pro Gly Val Gly Ser Glu Glu
 675 680 685

gcc cca gag ctg tgc ccg caa cat agc ccc ctg gat gcg acg ccc cac
 2112
 Ala Pro Glu Leu Cys Pro Gln His Ser Pro Leu Asp Ala Thr Pro His
 690 695 700

acc ctg gtg cag ccc atc ccc gcc acg ctg gct tcc gat ccc gcc agc
 2160
 Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala Ser Asp Pro Ala Ser
 705 710 715 720

tgc cct tgc tgc cag cat gag gac ggc cgg cgg ccc tcg ggc ctg ggc
 2208

Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg Pro Ser Gly Leu Gly
 725 730 735
 agc acc gac tcg ggc cag gag ggc tcg ggc tcc ggg agc tcc gct ggt
 2256
 Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Ser Ser Ala Gly
 740 745 750
 ggc gag gac gag gcg gat ggg gac ggg gcc cgg agc agc gag gac gga
 2304
 Gly Glu Asp Glu Ala Asp Gly Asp Gly Ala Arg Ser Ser Glu Asp Gly
 755 760 765
 gcc tcc tca gaa ctg ggg aag gag gag gag gag gag gag cag gcg gat
 2352
 Ala Ser Ser Glu Leu Gly Lys Glu Glu Glu Glu Glu Glu Gln Ala Asp
 770 775 780
 ggg gcg gtc tgg ctg tgc ggg gat gtg tgg cgg gag acg cga gcc aag
 2400
 Gly Ala Val Trp Leu Cys Gly Asp Val Trp Arg Glu Thr Arg Ala Lys
 785 790 795 800
 ctg cgc ggc atc gtg gac agc aag tac ttc aac cgg ggc atc atg atg
 2448
 Leu Arg Gly Ile Val Asp Ser Lys Tyr Phe Asn Arg Gly Ile Met Met
 805 810 815
 gcc atc ctg gtc aac acc gtc agc atg ggc atc gag cac cac gag cag
 2496
 Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile Glu His His Glu Gln
 820 825 830
 gcc agt gca gcg cag ccg ggc cgg gcc tgc ggg aga gga caa aat cca
 2544
 Ala Ser Ala Ala Gln Pro Gly Arg Ala Cys Gly Arg Gly Gln Asn Pro
 835 840 845
 gac ctt tgc atg acc ctc aag gcc cct tgt ctc tgt cac aac gtc cct
 2592
 Asp Leu Cys Met Thr Leu Lys Ala Pro Cys Leu Cys His Asn Val Pro
 850 855 860
 tca cca ggc cag ggt gtc ctg tcc cat cca gtg act cca ccc cat aca
 2640
 Ser Pro Gly Gln Gly Val Leu Ser His Pro Val Thr Pro Pro His Thr
 865 870 875 880
 gcc cca tgg cgc atg gag aca gga aag cag gga cac gga tgt gaa gaa
 2688
 Ala Pro Trp Arg Met Glu Thr Gly Lys Gln Gly His Gly Cys Glu Glu
 885 890 895
 gga cca gga caa cga agc agt gac atg ttt gcc ctg gag atg atc ctg
 2736
 Gly Pro Gly Gln Arg Ser Ser Asp Met Phe Ala Leu Glu Met Ile Leu
 900 905 910

aag ctg gct gca ttt ggg ctc ttc gac tac ctg cgt aac ccc tac aac
2784
Lys Leu Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn
915 920 925

atc ttc gac agc atc att gtc atc atc agc atc tgg gag atc gtg ggg
2832
Ile Phe Asp Ser Ile Ile Val Ile Ile Ser Ile Trp Glu Ile Val Gly
930 935 940

cag gcg gac ggt ggg ctg tcg gtg ctg cgg acc ttc cgg ctg ctg cgc
2880
Gln Ala Asp Gly Gly Leu Ser Val Leu Arg Thr Phe Arg Leu Leu Arg
945 950 955 960

gtg ctg aaa ctg gtg cgc ttc atg cct gcc ctg cgg cgc cag ctc gtg
2928
Val Leu Lys Leu Val Arg Phe Met Pro Ala Leu Arg Arg Gln Leu Val
965 970 975

gtg ctc atg aag acc atg gac aac gtg gcc acc ttc tgc atg ctg ctc
2976
Val Leu Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu
980 985 990

atg ctc ttc atc ttc atc ttc agc atc ctt ggg atg cat att ttt ggc
3024
Met Leu Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly
995 1000 1005

tgc aag ttc agc ctc cgc acg gac act gga gac acg gtg ccc gac agg
3072
Cys Lys Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg
1010 1015 1020

aag aac ttc gac tcc ctg ctg tgg gcc atc gtc act gtg ttc cag atc
3120
Lys Asn Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile
1025 1030 1035 1040

ctc acc cag gag gac tgg aac gtc gtt ctc tac aat ggc atg gcc tcc
3168
Leu Thr Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser
1045 1050 1055

act tct ccc tgg gcc tcc ctc tac ttt gtc gcc ctc atg acc ttc ggc
3216
Thr Ser Pro Trp Ala Ser Leu Tyr Phe Val Ala Leu Met Thr Phe Gly
1060 1065 1070

aac tat gtg ctc ttc aac ctg ctg gtg gcc atc ctg gtg gag ggc ttc
3264
Asn Tyr Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val Glu Gly Phe
1075 1080 1085

cag gcg gag gtg act gtg gtc ttg gca gag gaa gca ccc cca cag ggc
 3312
 Gln Ala Glu Val Thr Val Val Leu Ala Glu Glu Ala Pro Pro Gln Gly
 1090 1095 1100

 ctg cga aag act ggg cga ggg aga ggt ggc ctg gat ggg gga ggg ctg
 3360
 Leu Arg Lys Thr Gly Arg Gly Arg Gly Gly Leu Asp Gly Gly Gly Leu
 1105 1110 1115 1120

 caa ttc aaa ctt cta gca ggc aac cta tcc cta aag gag ggg gtt gct
 3408
 Gln Phe Lys Leu Leu Ala Gly Asn Leu Ser Leu Lys Glu Gly Val Ala
 1125 1130 1135

 gat gag gtg ggt gac gcc aat cgc tcc tac tcg gac gag gac cag agc
 3456
 Asp Glu Val Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser
 1140 1145 1150

 tca tcc aac ata gaa gag ttt gat aag ctc cag gaa ggc ctg gac agc
 3504
 Ser Ser Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser
 1155 1160 1165

 agc gga gat ccc aag ctc tgc cca atc ccc atg acc ccc aat ggg cac
 3552
 Ser Gly Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Gly His
 1170 1175 1180

 ctg gac ccc agt ctc cca ctg ggt ggg cac cta ggt cct gct ggg gct
 3600
 Leu Asp Pro Ser Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala
 1185 1190 1195 1200

 gcg gga cct gcc ccc cga ctc tca ctg cag ccg gac ccc atg ctg gtg
 3648
 Ala Gly Pro Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro Met Leu Val
 1205 1210 1215

 gcc ctg ggc tcc cga aag agc agc gtc atg tct cta ggg agg atg agc
 3696
 Ala Leu Gly Ser Arg Lys Ser Ser Val Met Ser Leu Gly Arg Met Ser
 1220 1225 1230

 tat gac cag cgc tcc ctg gtg ggt ggt ctt aga gcc aca gcg ggg gtg
 3744
 Tyr Asp Gln Arg Ser Leu Val Gly Gly Leu Arg Ala Thr Ala Gly Val
 1235 1240 1245

 cag gct gcc ttt ggg cac ctg gtg ccc cag ccg tgg gtg tgc ctg tgg
 3792
 Gln Ala Ala Phe Gly His Leu Val Pro Gln Pro Trp Val Cys Leu Trp
 1250 1255 1260

 ggc gct gac ccg aac ggg aac tcc ttc cag tcc agc tcc cgg agc tcc
 3840

Gly Ala Asp Pro Asn Gly Asn Ser Phe Gln Ser Ser Ser Arg Ser Ser
 1265 1270 1275 1280
 tac tac ggg cca tgg ggc cgc agc gcg gcc tgg gcc agc cgt cgc tcc
 3888
 Tyr Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser
 1285 1290 1295
 agc tgg aac agc ctc aag cac aag ccg ccg tcg gcg gag cat gag tcc
 3936
 Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser
 1300 1305 1310
 ctg ctc tct gcg gag cgc ggc ggc ggc gcc cgg gtc tgc gag gtt gcc
 3984
 Leu Leu Ser Ala Glu Arg Gly Gly Gly Ala Arg Val Cys Glu Val Ala
 1315 1320 1325
 gcg gac gag ggg ccg ccg cgg gcc gca ccc ctg cac acc cca cac gcc
 4032
 Ala Asp Glu Gly Pro Pro Arg Ala Ala Pro Leu His Thr Pro His Ala
 1330 1335 1340
 cac cac gtt cat cac ggg ccc cat ctg gcg cac cgc cac cgc cac cac
 4080
 His His Val His His Gly Pro His Leu Ala His Arg His Arg His His
 1345 1350 1355 1360
 cgc cgg acg ctg tcc ctc gac aac agg gac tcg gtg gac ctg gcc gag
 4128
 Arg Arg Thr Leu Ser Leu Asp Asn Arg Asp Ser Val Asp Leu Ala Glu
 1365 1370 1375
 ctg gtg ccc gcg gtg ggc gcc cac ccc cgg gcc gcc tgg agg gcg gca
 4176
 Leu Val Pro Ala Val Gly Ala His Pro Arg Ala Ala Trp Arg Ala Ala
 1380 1385 1390
 ggc ccg gcc ccc ggg cat gag gac tgc aat ggc agg atg ccc agc atc
 4224
 Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly Arg Met Pro Ser Ile
 1395 1400 1405
 gcc aaa gac gtc ttc acc aag atg ggc gac cgc ggg gat cgc ggg gag
 4272
 Ala Lys Asp Val Phe Thr Lys Met Gly Asp Arg Gly Asp Arg Gly Glu
 1410 1415 1420
 gat gag gag gaa atc gac tac gtg agt ggg ggc ggg gcc gaa ggg gac
 4320
 Asp Glu Glu Glu Ile Asp Tyr Val Ser Gly Gly Gly Ala Glu Gly Asp
 1425 1430 1435 1440
 ctg acc ctg tgc ttc cgc gtc cgc aag atg atc gac gtc tat aag ccc
 4368
 Leu Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro
 1445 1450 1455

gac tgg tgc gag gtc cgc gaa gac tgg tct gtc tac ctc ttc tct ccc
 4416
 Asp Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro
 1460 1465 1470

gag aac agg ctc agg gat ctg ggc tgg gta agc ctc gag tgc cag gga
 4464
 Glu Asn Arg Leu Arg Asp Leu Gly Trp Val Ser Leu Glu Cys Gln Gly
 1475 1480 1485

aag gtg ggt gac ctc gtg gtg tgg gtg tat ggt cag agg agg cag cgc
 4512
 Lys Val Gly Asp Leu Val Val Trp Val Tyr Gly Gln Arg Arg Gln Arg
 1490 1495 1500

cag acc att att gcc cac aaa ctc ttc gac tac gtc gtc ctg gcc ttc
 4560
 Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu Ala Phe
 1505 1510 1515 1520

atc ttt ctc aac tgc atc acc atc gcc ctg gag cgg cct cag atc gag
 4608
 Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln Ile Glu
 1525 1530 1535

gcc ggc agc acc gaa cgc atc ttt ctc acc gtg tcc aac tac atc ttc
 4656
 Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe
 1540 1545 1550

acg gcc atc ttc gtg ggc gag atg aca ttg aag gta gtc tcg ctg ggc
 4704
 Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly
 1555 1560 1565

ctg tac ttc ggc gag cag gcg tac cta cgc agc agc tgg aac gtg ctg
 4752
 Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
 1570 1575 1580

gat ggc ttt ctt gtc ttc gtg tcc atc atc gac atc gtg gtg tcc ctg
 4800
 Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Leu
 1585 1590 1595 1600

gcc tca gcc ggg gga gcc aag atc ttg ggg gtc ctc cga gtc ttg cgg
 4848
 Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val Leu Arg
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ctc ctg cgc acc cta cgc ccc ctg cgt gtc atc agc cgg gcg ccg ggc
 4896
 Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly
 1620 1625 1630

ctg aag ctg gtg gtg gag aca ctc atc tcc tcc ctc aag ccc atc ggc
 4944
 Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly
 1635 1640 1645

 aac atc gtg ctc atc tgc tgt gcc ttc ttc atc atc ttt ggc atc ctg
 4992
 Asn Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
 1650 1655 1660

 gga gtg cag ctc ttc aag ggc aag ttc tac cac tgt ctg ggc gtg gac
 5040
 Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp
 1665 1670 1675 1680

 acc cgc aac atc acc aac cgc tcg gac tgc atg gcc gcc aac tac cgc
 5088
 Thr Arg Asn Ile Thr Asn Arg Ser Asp Cys Met Ala Ala Asn Tyr Arg
 1685 1690 1695

 tgg gtc cat cac aaa tac aac ttc gac aac ctg ggc cag gct ctg atg
 5136
 Trp Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
 1700 1705 1710

 tcc ctc ttt gtc ctg gca tcc aag gat ggt tgg gtg aac atc atg tac
 5184
 Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr
 1715 1720 1725

 aat gga ctg gat gct gtt gct gtg gac cag cag cct gtg acc aac cac
 5232
 Asn Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His
 1730 1735 1740

 aac ccc tgg atg ctg ctg tac ttc atc tcc ttc ctg ctc atc gtc agc
 5280
 Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser
 1745 1750 1755 1760

 ttc ttt gtg ctc aac atg ttt gtg ggt gtc gtg gtg gag aac ttc cac
 5328
 Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
 1765 1770 1775

 aag tgc cgg cag cac cag gag gct gaa gag gca cgg cgg cgt gag gag
 5376
 Lys Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu
 1780 1785 1790

 aag cgg ctg cgg cgc ctg gag aag aag cgc cgg aag gcc cag cgg ctg
 5424
 Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Arg Leu
 1795 1800 1805

 ccc tac tat gcc acc tat tgt cac acc cgg ctg ctc atc cac tcc atg
 5472

Pro Tyr Tyr Ala Thr Tyr Cys His Thr Arg Leu Leu Ile His Ser Met
 1810 1815 1820

tgc acc agc cac tac ctg gac atc ttc atc acc ttc atc atc tgc ctc
 5520

Cys Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile Cys Leu
 1825 1830 1835 1840

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 5562

Asn Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
 1845 1850

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 Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln
 35 40 45
 Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg Thr
 50 55 60
 His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met His
 65 70 75 80
 Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His Pro
 85 90 95
 Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr Gly
 100 105 110
 Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe Glu
 115 120 125
 Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met
 130 135 140
 Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys Ile
 145 150 155 160
 Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu Met
 165 170 175
 Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr Leu
 180 185 190
 Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly Asn
 195 200 205
 Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Lys
 210 215 220
 Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Asn Leu Leu Leu
 225 230 235 240
 Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val
 245 250 255
 Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala Gly Leu Leu
 260 265 270
 Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp Val
 275 280 285
 Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro Phe

290		295		300
Ile Cys Ser Leu Ser Gly Asp Asn Gly Ile Met Gly Cys His Glu Ile				
305		310		315
Pro Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp Asp				320
		325		330
Val Tyr Asp Phe Gly Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly Leu				335
		340		345
Cys Val Asn Trp Asn Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser Ala				350
		355		360
Asn Pro His Lys Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp				365
		370		375
Ile Val Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met				380
385		390		395
Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile				400
		405		410
Leu Leu Ile Ile Ser Glu Leu Ile His Leu Val Met Pro Asp Cys Ser				415
		420		425
Phe Ser Thr Ala Gln Ser Pro Lys Cys Gln Gly Asp Ser Leu Pro Gly				430
		435		440
Val Ala Ala Glu Ser Leu Leu Leu Arg Asp Ser Ser Ser Ser Val Ile				445
		450		455
Thr Asp Glu Ala Ala Ala Met Glu Asn Leu Leu Ala Gly Thr Ser Lys				460
465		470		475
Gly Asp Glu Ser Tyr Leu Leu Arg Leu Ala Gly Ser Gln Val His Ser				480
		485		490
Gln Ala Gln Gln Met Leu Gly Arg Gly Leu Gly Pro Glu Ser Leu Glu				495
		500		505
Thr Gly Glu Glu Pro His Ser Trp Ser Pro Arg Ala Thr Arg Arg Trp				510
		515		520
Asp Pro Gln Cys Gln Pro Gly Gln Pro Leu Pro Leu His Phe Met Gln				525
		530		535
Ala Gln Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile				540
545		550		555
Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu				560
		565		570
Glu Gln Arg Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala				575
		580		585
Glu Pro Gly Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile				590
		595		600
Leu Arg Lys Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln				605
		610		615
Ser Arg Arg Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys Pro				620
625		630		635
Gly Pro His Ala Lys Glu Pro Arg His Tyr Pro Leu Thr Val Trp Glu				640
		645		650
Ser Ile Leu Gly Arg Gln Ala Glu Glu Cys Thr Leu Arg Ala Ala Ala				655
		660		665
His Pro Ser Ser Gly Ala Ser His Pro Gly Val Gly Ser Glu Glu Ala				670
		675		680
Pro Glu Leu Cys Pro Gln His Ser Pro Leu Asp Ala Thr Pro His Thr				685
		690		695
Leu Val Gln Pro Ile Pro Ala Thr Leu Ala Ser Asp Pro Ala Ser Cys				700
705		710		715
Pro Cys Cys Gln His Glu Asp Gly Arg Arg Pro Ser Gly Leu Gly Ser				720
		725		730
Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Ser Ser Ala Gly Gly				735
		740		745
				750

Glu	Asp	Glu	Ala	Asp	Gly	Asp	Gly	Ala	Arg	Ser	Ser	Glu	Asp	Gly	Ala	755	760	765
Ser	Ser	Glu	Leu	Gly	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Ala	Asp	Gly	770	775	780
Ala	Val	Trp	Leu	Cys	Gly	Asp	Val	Trp	Arg	Glu	Thr	Arg	Ala	Lys	Leu	785	790	800
Arg	Gly	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Asn	Arg	Gly	Ile	Met	Met	Ala	805	810	815
Ile	Leu	Val	Asn	Thr	Val	Ser	Met	Gly	Ile	Glu	His	His	Glu	Gln	Ala	820	825	830
Ser	Ala	Ala	Gln	Pro	Gly	Arg	Ala	Cys	Gly	Arg	Gly	Gln	Asn	Pro	Asp	835	840	845
Leu	Cys	Met	Thr	Leu	Lys	Ala	Pro	Cys	Leu	Cys	His	Asn	Val	Pro	Ser	850	855	860
Pro	Gly	Gln	Gly	Val	Leu	Ser	His	Pro	Val	Thr	Pro	Pro	His	Thr	Ala	865	870	875
Pro	Trp	Arg	Met	Glu	Thr	Gly	Lys	Gln	Gly	His	Gly	Cys	Glu	Glu	Gly	885	890	895
Pro	Gly	Gln	Arg	Ser	Ser	Asp	Met	Phe	Ala	Leu	Glu	Met	Ile	Leu	Lys	900	905	910
Leu	Ala	Ala	Phe	Gly	Leu	Phe	Asp	Tyr	Leu	Arg	Asn	Pro	Tyr	Asn	Ile	915	920	925
Phe	Asp	Ser	Ile	Ile	Val	Ile	Ile	Ser	Ile	Trp	Glu	Ile	Val	Gly	Gln	930	935	940
Ala	Asp	Gly	Gly	Leu	Ser	Val	Leu	Arg	Thr	Phe	Arg	Leu	Leu	Arg	Val	945	950	955
Leu	Lys	Leu	Val	Arg	Phe	Met	Pro	Ala	Leu	Arg	Arg	Gln	Leu	Val	Val	965	970	975
Leu	Met	Lys	Thr	Met	Asp	Asn	Val	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	980	985	990
Leu	Phe	Ile	Phe	Ile	Phe	Ser	Ile	Leu	Gly	Met	His	Ile	Phe	Gly	Cys	995	1000	1005
Lys	Phe	Ser	Leu	Arg	Thr	Asp	Thr	Gly	Asp	Thr	Val	Pro	Asp	Arg	Lys	1010	1015	1020
Asn	Phe	Asp	Ser	Leu	Leu	Trp	Ala	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	1025	1030	1035
Thr	Gln	Glu	Asp	Trp	Asn	Val	Val	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	1045	1050	1055
Ser	Pro	Trp	Ala	Ser	Leu	Tyr	Phe	Val	Ala	Leu	Met	Thr	Phe	Gly	Asn	1060	1065	1070
Tyr	Val	Leu	Phe	Asn	Leu	Leu	Val	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	1075	1080	1085
Ala	Glu	Val	Thr	Val	Val	Leu	Ala	Glu	Glu	Ala	Pro	Pro	Gln	Gly	Leu	1090	1095	1100
Arg	Lys	Thr	Gly	Arg	Gly	Arg	Gly	Gly	Leu	Asp	Gly	Gly	Gly	Leu	Gln	1105	1110	1115
Phe	Lys	Leu	Leu	Ala	Gly	Asn	Leu	Ser	Leu	Lys	Glu	Gly	Val	Ala	Asp	1125	1130	1135
Glu	Val	Gly	Asp	Ala	Asn	Arg	Ser	Tyr	Ser	Asp	Glu	Asp	Gln	Ser	Ser	1140	1145	1150
Ser	Asn	Ile	Glu	Glu	Phe	Asp	Lys	Leu	Gln	Glu	Gly	Leu	Asp	Ser	Ser	1155	1160	1165
Gly	Asp	Pro	Lys	Leu	Cys	Pro	Ile	Pro	Met	Thr	Pro	Asn	Gly	His	Leu	1170	1175	1180
Asp	Pro	Ser	Leu	Pro	Leu	Gly	Gly	His	Leu	Gly	Pro	Ala	Gly	Ala	Ala	1185	1190	1195
Gly	Pro	Ala	Pro	Arg	Leu	Ser	Leu	Gln	Pro	Asp	Pro	Met	Leu	Val	Ala			1200

	1205		1210		1215
Leu Gly Ser Arg Lys Ser Ser Val Met Ser Leu Gly Arg Met Ser Tyr					
	1220		1225		1230
Asp Gln Arg Ser Leu Val Gly Gly Leu Arg Ala Thr Ala Gly Val Gln					
	1235		1240		1245
Ala Ala Phe Gly His Leu Val Pro Gln Pro Trp Val Cys Leu Trp Gly					
	1250		1255		1260
Ala Asp Pro Asn Gly Asn Ser Phe Gln Ser Ser Ser Arg Ser Ser Tyr					
1265		1270		1275	1280
Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser Ser					
	1285		1290		1295
Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser Leu					
	1300		1305		1310
Leu Ser Ala Glu Arg Gly Gly Gly Ala Arg Val Cys Glu Val Ala Ala					
	1315		1320		1325
Asp Glu Gly Pro Pro Arg Ala Ala Pro Leu His Thr Pro His Ala His					
	1330		1335		1340
His Val His His Gly Pro His Leu Ala His Arg His Arg His His Arg					
1345		1350		1355	1360
Arg Thr Leu Ser Leu Asp Asn Arg Asp Ser Val Asp Leu Ala Glu Leu					
	1365		1370		1375
Val Pro Ala Val Gly Ala His Pro Arg Ala Ala Trp Arg Ala Ala Gly					
	1380		1385		1390
Pro Ala Pro Gly His Glu Asp Cys Asn Gly Arg Met Pro Ser Ile Ala					
	1395		1400		1405
Lys Asp Val Phe Thr Lys Met Gly Asp Arg Gly Asp Arg Gly Glu Asp					
	1410		1415		1420
Glu Glu Glu Ile Asp Tyr Val Ser Gly Gly Gly Ala Glu Gly Asp Leu					
1425		1430		1435	1440
Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp					
	1445		1450		1455
Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro Glu					
	1460		1465		1470
Asn Arg Leu Arg Asp Leu Gly Trp Val Ser Leu Glu Cys Gln Gly Lys					
	1475		1480		1485
Val Gly Asp Leu Val Val Trp Val Tyr Gly Gln Arg Arg Gln Arg Gln					
	1490		1495		1500
Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu Ala Phe Ile					
1505		1510		1515	1520
Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln Ile Glu Ala					
	1525		1530		1535
Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe Thr					
	1540		1545		1550
Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly Leu					
	1555		1560		1565
Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp					
	1570		1575		1580
Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Leu Ala					
1585		1590		1595	1600
Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val Leu Arg Leu					
	1605		1610		1615
Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly Leu					
	1620		1625		1630
Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly Asn					
	1635		1640		1645
Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly					
	1650		1655		1660

Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp Thr
 1665 1670 1675 1680
 Arg Asn Ile Thr Asn Arg Ser Asp Cys Met Ala Ala Asn Tyr Arg Trp
 1685 1690 1695
 Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser
 1700 1705 1710
 Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr Asn
 1715 1720 1725
 Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His Asn
 1730 1735 1740
 Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser Phe
 1745 1750 1755 1760
 Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys
 1765 1770 1775
 Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu Lys
 1780 1785 1790
 Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Arg Leu Pro
 1795 1800 1805
 Tyr Tyr Ala Thr Tyr Cys His Thr Arg Leu Leu Ile His Ser Met Cys
 1810 1815 1820
 Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile Cys Leu Asn
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 Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
 1845 1850

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 <212> DNA
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 <223> Human alpha-1 partial sequence

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 aat gtc ctg ctg ctc tgc ttc ttt gtc ttc ttc acc ttt ggc atc ata
 96
 Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Thr Phe Gly Ile Ile
 20 25 30
 ggt gtg cag ctc tgg gcg ggc ctg ctg cgt aac cgc tgc ttc ctg gag
 144
 Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
 35 40 45
 gag aac ttc acc ata caa ggg gat gtg gcc ttg ccc cca tac tac cag
 192
 Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
 50 55 60

ccg gag gag gat gat gag atg ccc ttc atc tgc tcc ctg tcg ggc gac
 240
 Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser Gly Asp
 65 70 75 80

aat ggg ata atg ggc tgc cat gag atc ccc ccg ctc aag gag cag ggc
 288
 Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
 85 90 95

cgt gag tgc tgc ctg tcc aag gac gac gtc tac gac ttt ggg gcg ggg
 336
 Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
 100 105 110

cgc cag gac ctc aat gcc agc ggc ctc tgt gtc aac tgg aac cgt tac
 384
 Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
 115 120 125

tac aat gtg tgc cgc acg ggc agc gcc aac ccc cac aag ggt gcc atc
 432
 Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly Ala Ile
 130 135 140

agc ttt gac aac atc ggt tat gct tgg att gtc atc ttc cag gtg atc
 480
 Ser Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile
 145 150 155 160

act ctg gaa ggc tgg gtg gcg atc atg tac tac gtg atg gat gct ctc
 528
 Thr Leu Glu Gly Trp Val Ala Ile Met Tyr Tyr Val Met Asp Ala Leu
 165 170 175

tcc ttc tac aac ttc gtc tac ttc atc ctg ctt atc ata
 567
 Ser Phe Tyr Asn Phe Val Tyr Phe Ile Leu Leu Ile Ile
 180 185

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 <212> PRT
 <213> Human

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 35 40 45
 Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln Pro
 50 55 60
 Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser Gly Asp Asn
 65 70 75 80

Gly	Ile	Met	Gly	Cys	His	Glu	Ile	Pro	Pro	Leu	Lys	Glu	Gln	Gly	Arg
			85						90					95	
Glu	Cys	Cys	Leu	Ser	Lys	Asp	Asp	Val	Tyr	Asp	Phe	Gly	Ala	Gly	Arg
			100					105					110		
Gln	Asp	Leu	Asn	Ala	Ser	Gly	Leu	Cys	Val	Asn	Trp	Asn	Arg	Tyr	Tyr
		115					120					125			
Asn	Val	Cys	Arg	Thr	Gly	Ser	Ala	Asn	Pro	His	Lys	Gly	Ala	Ile	Ser
	130					135					140				
Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Val	Ile	Phe	Gln	Val	Ile	Thr
145					150					155					160
Leu	Glu	Gly	Trp	Val	Ala	Ile	Met	Tyr	Tyr	Val	Met	Asp	Ala	Leu	Ser
				165					170					175	
Phe	Tyr	Asn	Phe	Val	Tyr	Phe	Ile	Leu	Leu	Ile	Ile				
			180					185							

<210> 22

<211> 567

<212> DNA

<213> Rat

<220>

<221> CDS

<222> (1)...(567)

<223> Rat alpha-1 partial sequence

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Met	Arg	Ile	Leu	Val	Asn	Leu	Leu	Leu	Asp	Thr	Leu	Pro	Met	Leu	Gly
1				5					10					15	

aac gtg ctc ctg ctc tgt ttc ttc gtc ttc ttc atc ttc ggc atc att
96

Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile	Phe	Gly	Ile	Ile
			20					25					30		

ggc gtg cag ctc tgg gca ggc ctg cta cgg aac cgc tgc ttc ctg gaa
144

Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg	Cys	Phe	Leu	Glu
		35					40					45			

gaa aac ttc acc ata caa ggg gat gtg gcc ctg ccc cct tat tac caa
192

Glu	Asn	Phe	Thr	Ile	Gln	Gly	Asp	Val	Ala	Leu	Pro	Pro	Tyr	Tyr	Gln
	50					55						60			

cca gag gag gat gac gag atg ccc ttt atc tgc tcc ctg act ggg gac
240

Pro	Glu	Glu	Asp	Asp	Glu	Met	Pro	Phe	Ile	Cys	Ser	Leu	Thr	Gly	Asp
	65					70				75				80	

aat ggc atc atg ggc tgc cac gag atc ccc cca ctg aag gag cag ggc
288

Asn	Gly	Ile	Met	Gly	Cys	His	Glu	Ile	Pro	Pro	Leu	Lys	Glu	Gln	Gly
				85					90					95	

cgg gaa tgc tgc ctg tcc aaa gat gat gtg tat gac ttc ggg gcg ggg
 336
 Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
 100 105 110

cgc cag gac ctc aac gcc agc ggt ctg tgc gtc aac tgg aac cgc tac
 384
 Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
 115 120 125

tac aac gtc tgc cgc acg ggc aac gcc aac cct cac aag ggc gcc atc
 432
 Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile
 130 135 140

aac ttt gac aac att ggc tat gcc tgg att gtg att ttc cag gtg atc
 480
 Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile
 145 150 155 160

act ctg gaa ggc tgg gtg gag atc atg tac tat gtg atg gac gca cat
 528
 Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His
 165 170 175

tct ttc tac aac ttc atc tac ttc atc ctg ctt atc ata
 567
 Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile
 180 185

<210> 23
 <211> 188
 <212> PRT
 <213> Rat

<400> 23
 Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met Leu Gly Asn
 1 5 10 15
 Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile Gly
 20 25 30
 Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu Glu
 35 40 45
 Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln Pro
 50 55 60
 Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp Asn
 65 70 75 80
 Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly Arg
 85 90 95
 Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly Arg
 100 105 110
 Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr Tyr
 115 120 125
 Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile Asn
 130 135 140
 Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile Thr
 145 150 155 160

Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His Ser
 165 170 175
 Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile
 180 185

<210> 24
 <211> 31
 <212> PRT
 <213> Human

<400> 24
 Val Ile Ser Leu Glu Gly Trp Thr Asp Ile Met Tyr Tyr Val Gln Asp
 1 5 10 15
 Ala His Ser Phe Trp Asn Trp Ile Tyr Phe Val Leu Leu Ile Val
 20 25 30

<210> 25
 <211> 31
 <212> PRT
 <213> C. elegans

<400> 25
 Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp
 1 5 10 15
 Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile
 20 25 30

<210> 26
 <211> 23
 <212> PRT
 <213> Human

<400> 26
 Asn Ile Asn Leu Thr Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
 1 5 10 15
 Arg Ala Val Asn Arg Ile Pro
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<210> 27
 <211> 23
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 <213> C. elegans

<400> 27
 Asn Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
 1 5 10 15
 Lys Ala Ile Asn Arg Val Pro
 20

<210> 28
 <211> 19
 <212> PRT
 <213> Human

<400> 28
 Met Ala Val Ile Met Ile Asn Cys Val Thr Leu Gly Met Tyr Arg Pro
 1 5 10 15

Cys Glu Asp

<210> 29

<211> 19

<212> PRT

<213> C. elegans

<400> 29

Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met Tyr Gln Pro
1 5 10 15

Cys Asp Asp

<210> 30

<211> 23

<212> PRT

<213> Human

<400> 30

Leu Thr Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Val
1 5 10 15

Asn Arg Ile Pro Ser Met Arg
20

<210> 31

<211> 23

<212> PRT

<213> C. elegans

<400> 31

Ile Lys Ser Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu
1 5 10 15

Ser Arg Phe Glu Gly Met Arg
20

<210> 32

<211> 41

<212> PRT

<213> Human

<400> 32

Pro Thr Ile Ile Arg Val Met Arg Val Leu Arg Ile Ala Arg Val Leu
1 5 10 15

Lys Leu Leu Lys Met Ala Lys Gly Ile Arg Ser Leu Leu Asp Thr Val
20 25 30

Gly Glu Ala Leu Pro Gln Val Gly Asn
35 40

<210> 33

<211> 40

<212> PRT

<213> C. elegans

<220>

<221> VARIANT

<222> (1) ... (40)

<223> Xaa = Any Amino Acid

<400> 33

Pro	Thr	Leu	Xaa	Arg	Val	Ile	Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu
1				5					10					15	
Arg	Leu	Ile	Lys	Ala	Lys	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	Met
			20					25					30		
Met	Ser	Leu	Pro	Ala	Leu	Phe	Asn								
		35					40								